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1646

RAW SEQUENCE LISTING

DATE: 02/11/2002

PATENT APPLICATION: US/09/899,429A

TIME: 13:40:42

Input Set : A:\98385Jseq.txt

Output Set: N:\CRF3\02112002\I899429A.raw

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TECH CENTER 1600/2900

ENTERED

3 <110> APPLICANT: Hauptmann, Rudolph
4 Himmeler, Adolph
5 Maurer-Fogy, Ingrid
6 Stratowa, Christian
8 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
9 Them
11 <130> FILE REFERENCE: 98-385-J
13 <140> CURRENT APPLICATION NUMBER: 09/899,429A
14 <141> CURRENT FILING DATE: 2001-07-03
16 <150> PRIOR APPLICATION NUMBER: 09/792,356
17 <151> PRIOR FILING DATE: 2000-02-23
19 <150> PRIOR APPLICATION NUMBER: 08/477,639
20 <151> PRIOR FILING DATE: 1955-06-07
22 <150> PRIOR APPLICATION NUMBER: 08/383,676
23 <151> PRIOR FILING DATE: 1995-02-01
25 <150> PRIOR APPLICATION NUMBER: 08/153,287
26 <151> PRIOR FILING DATE: 1993-11-17
28 <150> PRIOR APPLICATION NUMBER: 07/821,750
29 <151> PRIOR FILING DATE: 1992-01-02
31 <150> PRIOR APPLICATION NUMBER: 07/511,430
32 <151> PRIOR FILING DATE: 1990-04-20
34 <160> NUMBER OF SEQ ID NOS: 97
36 <170> SOFTWARE: PatentIn Ver. 2.0
38 <210> SEQ ID NO: 1
39 <211> LENGTH: 1368
40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
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44 <221> NAME/KEY: CDS
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47 <220> FEATURE:
48 <221> NAME/KEY: sig_peptide
49 <222> LOCATION: (1)..(87)
51 <220> FEATURE:
52 <221> NAME/KEY: misc_feature
53 <222> LOCATION: (88)..(120)
54 <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
55 extracellular proteases following secretion
57 <220> FEATURE:
58 <221> NAME/KEY: misc_feature
59 <222> LOCATION: (606)..(633)
60 <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
61 extracellular proteases following secretion

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63 <400> SEQUENCE: 1

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65 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
66 1 5 10 15
68 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct 96
69 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
70 20 25 30
72 cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa 144
73 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
74 35 40 45
76 tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa 192
77 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
78 50 55 60
80 gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac 240
81 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
82 65 70 75 80
84 tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc 288
85 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
86 85 90 95
88 aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg 336
89 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
90 100 105 110
92 gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg 384
93 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
94 115 120 125
96 aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc 432
97 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
98 130 135 140
100 aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag 480
101 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
102 145 150 155 160
104 aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa 528
105 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
106 165 170 175
108 aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg 576
109 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
110 180 185 190
112 aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca 624
113 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
114 195 200 205
116 ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt 672
117 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
118 210 215 220
120 tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag 720
121 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
122 225 230 235 240
124 tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag 768
125 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
126 245 250 255

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128 ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc 816
129 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
130      260      265      270
132 ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg 864
133 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
134      275      280      285
136 ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt 912
137 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
138      290      295      300
140 ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca cca tat cag ggg 960
141 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
142 305      310      315      320
144 gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac 1008
145 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
146      325      330      335
148 ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac 1056
149 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
150      340      345      350
152 act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg 1104
153 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
154      355      360      365
156 ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag 1152
157 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
158      370      375      380
160 atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa 1200
161 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
162 385      390      395      400
164 tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc 1248
165 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
166      405      410      415
168 acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc 1296
169 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
170      420      425      430
172 tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg 1344
173 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
174      435      440      445
176 ccc gcg ccc agt ctt ctc aga tga 1368
177 Pro Ala Pro Ser Leu Leu Arg
178      450      455
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 455
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 2
187 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
188 1      5      10      15
190 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
191      20      25      30
193 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys

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194	35	40	45
196	Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys		
197	50	55	60
199	Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp		
200	65	70	75
202	Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu		
203	85	90	95
205	Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val		
206	100	105	110
208	Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg		
209	115	120	125
211	Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe		
212	130	135	140
214	Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu		
215	145	150	155
217	Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu		
218	165	170	175
220	Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr		
221	180	185	190
223	Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser		
224	195	200	205
226	Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu		
227	210	215	220
229	Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys		
230	225	230	235
232	Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu		
233	245	250	255
235	Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser		
236	260	265	270
238	Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val		
239	275	280	285
241	Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys		
242	290	295	300
244	Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly		
245	305	310	315
247	Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn		
248	325	330	335
250	Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp		
251	340	345	350
253	Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro		
254	355	360	365
256	Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu		
257	370	375	380
259	Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln		
260	385	390	395
262	Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala		
263	405	410	415
265	Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly		
266	420	425	430

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269          435                      440                      445
271 Pro Ala Pro Ser Leu Leu Arg
272    450                      455
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276 <211> LENGTH: 483
277 <212> TYPE: DNA
278 <213> ORGANISM: Homo sapiens
280 <220> FEATURE:
281 <221> NAME/KEY: CDS
282 <222> LOCATION: (1)..(483)
284 <400> SEQUENCE: 3
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286 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
287   1          5          10          15
289 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt    96
290 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
291          20          25          30
293 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc    144
294 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
295          35          40          45
297 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa    192
298 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
299   50          55          60
301 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac    240
302 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
303  65          70          75          80
305 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg    288
306 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
307          85          90          95
309 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg    336
310 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
311          100          105          110
313 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc    384
314 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
315          115          120          125
317 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac    432
318 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
319          130          135          140
321 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag    480
322 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
323 145          150          155          160
325 aat    483
326 Asn
329 <210> SEQ ID NO: 4
330 <211> LENGTH: 161
331 <212> TYPE: PRT
332 <213> ORGANISM: Homo sapiens
334 <400> SEQUENCE: 4

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 02/11/2002

PATENT APPLICATION: US/09/899,429A

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Input Set : A:\98385Jseq.txt

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L:1494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:2357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:2432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:2473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:2476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:2495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:2498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:2531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46